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PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/980,381

DATE: 03/28/2002 8.5
TIME: 10:36:39

Input Set : A:\EP.txt

Output Set: N:\CRF3\03282002\I980381.raw

3 <110> APPLICANT: Zoghbi, Huda

4 Ben-Arie, Nissim

5 Bellen, Hugo

6 Bermingham, Nessim

7 Hassan, Bassem

9 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN
TONAL-ASSOCIATED

10 SEQUENCE FOR DEAFNESS, OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION

12 <130> FILE REFERENCE: HO-P01899US3/09906355/OTA 99-47

14 <140> CURRENT APPLICATION NUMBER: US 09/980,381

15 <141> CURRENT FILING DATE: 2002-03-06

17 <150> PRIOR APPLICATION NUMBER: US 60/137,060

18 <151> PRIOR FILING DATE: 1999-06-01

20 <150> PRIOR APPLICATION NUMBER: US 60/176,993

21 <151> PRIOR FILING DATE: 2000-01-19

23 <150> PRIOR APPLICATION NUMBER: PCT/US00/15410

24 <151> PRIOR FILING DATE: 2000-06-01

26 <160> NUMBER OF SEQ ID NOS: 69

28 <170> SOFTWARE: PatentIn version 3.0

30 <210> SEQ ID NO: 1

31 <211> LENGTH: 1065

32 <212> TYPE: DNA

33 <213> ORGANISM: HUMAN

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38 cgccagcccc agccgcatca tctcccgcaa ccgcccgcgc cgccgcagcc acctgcaact 120

40 ttgcaggcga gagagcatcc cgtctacccg cctgagctgt cctcctgga cagcaccgac 180

42 ccacgcgcct ggctggctcc cactttgcag ggcattctga cggcacgcgc cgcccagtat 240

44 ttgctacatt ccccgagct ggggtgcctca gaggcgctg cgccccggga cgaggtggac 300

46 ggccgggggg agctggtaag gagagcagc ggcggtgcc aagcagcaa gagccccggg 360

48 ccggtgaaag tgcgggaaca gctgtgcaag ctgaaaggcg ggggtggtgt agacgagctg 420

50 ggctgcagcc gccaacgggc ccttccagc aaacaggtga atggggtgca gaagcagaga 480

52 cggctagcag ccaacgccag ggagcggcgc aggatgcatg ggctgaacca cgccttcgac 540

54 cagctgcgca atgttatccc gtcgttcaac aacgacaaga agctgtccaa atatgagacc 600

56 ctgcagatgg cccaaatcta catcaacgcc ttgtccgagc tgctacaaac gccagcggga 660

58 ggggaacagc caccgcccgc tccagcctcc tgcaaaagcg accaccacca ccttcgcacc 720

60 gcggcctcct atgaaggggg cgcgggcaac gcgaccgcag ctggggctca gcaggcttcc 780

62 ggagggagcc agcggccgac cccgcccggg agttgcgga ctgccttctc agccccagct 840

64 tctgcgggag ggtactcgt gcagctggac gctctgact tctcgacttt cgaggacagc 900

66 gccctgacag cgaatgatgc gcaaaagaat ttgtctcctt ctctccccgg gagcatcttg 960

68 cagccagtgc aggaggaaaa cagcaaaact tcgctcggg cccacagaag cgacggggaa 1020

70 ttttcccccc attcccatta cagtactcgc gatgaggcaa gtttag 1065

73 <210> SEQ ID NO: 2

74 <211> LENGTH: 354

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75 <212> TYPE: PRT
76 <213> ORGANISM: HUMAN
78 <400> SEQUENCE: 2
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83 Gly Asp His His Arg Gln Pro Gln Pro His His Leu Pro Gln Pro Pro
84 20 25 30
86 Pro Pro Pro Gln Pro Pro Ala Thr Leu Gln Ala Arg Glu His Pro Val
87 35 40 45
89 Tyr Pro Pro Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp
90 50 55 60
92 Leu Ala Pro Thr Leu Gln Gly Ile Cys Thr Ala Arg Ala Ala Gln Tyr
93 65 70 75 80
95 Leu Leu His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg
96 85 90 95
98 Asp Glu Val Asp Gly Arg Gly Glu Leu Val Arg Arg Ser Ser Gly Gly
99 100 105 110
101 Ala Ser Ser Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu
102 115 120 125
104 Cys Lys Leu Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg
105 130 135 140
107 Gln Arg Ala Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg
108 145 150 155 160
110 Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Met His Gly Leu Asn
111 165 170 175
113 His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp
114 180 185 190
116 Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile
117 195 200 205
119 Asn Ala Leu Ser Glu Leu Leu Gln Thr Pro Ser Gly Gly Glu Gln Pro
120 210 215 220
122 Pro Pro Pro Pro Ala Ser Cys Lys Ser Asp His His His Leu Arg Thr
123 225 230 235 240
125 Ala Ala Ser Tyr Glu Gly Gly Ala Gly Asn Ala Thr Ala Ala Gly Ala
126 245 250 255
128 Gln Gln Ala Ser Gly Gly Ser Gln Arg Pro Thr Pro Pro Gly Ser Cys
129 260 265 270
131 Arg Thr Arg Phe Ser Ala Pro Ala Ser Ala Gly Gly Tyr Ser Val Gln
132 275 280 285
134 Leu Asp Ala Leu His Phe Ser Thr Phe Glu Asp Ser Ala Leu Thr Ala
135 290 295 300
137 Met Met Ala Gln Lys Asn Leu Ser Pro Ser Leu Pro Gly Ser Ile Leu
138 305 310 315 320
140 Gln Pro Val Gln Glu Asn Ser Lys Thr Ser Pro Arg Ser His Arg
141 325 330 335
143 Ser Asp Gly Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu
144 340 345 350
146 Ala Ser
149 <210> SEQ ID NO: 3

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150 <211> LENGTH: 420
151 <212> TYPE: DNA
152 <213> ORGANISM: MOUSE
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157 gcgggggacat tcccggacac acaccggagc agcagctgcg ccgcgacaca tctggagccg 120
159 cgtaggatgt tcgtcaaata tgagactctg gagttgaagg aggaagagga ggtactgatg 180
161 ctgctgggct cggttcccc ggctcggcg accctgacct cgatgtctc cagcgcggac 240
163 gaggaggagg acgaggagct gcgccggccg ggctccgcgc gtgggcagcg tggagcggaa 300
165 gccgggcagg ggggtgcagg cagtccggcg tcgggtgcct ggggttgccg gacagggcgg 360
167 ctgctatgca ctgtgcacga gtgctagcgt gtgccgtcgc gtcacgggc cgtctgcaga 420
170 <210> SEQ ID NO: 4
171 <211> LENGTH: 645
172 <212> TYPE: DNA
173 <213> ORGANISM: MOUSE
175 <400> SEQUENCE: 4
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178 tttcccgagg cctcggacca cgaagtgtc agttccaatt ccacccacc tagccccact 120
180 ctcataccta gggactgtc cgaagcagaa gtgggtgact gccgaggac ctcgaggaag 180
182 ctccgcgccc gacgcggagg gcgcaacagg cccaagagcg agttggcact cagcaaacag 240
184 cgaagaagcc ggcgcaagaa ggccaatgat cgggagcgca atcgcatgca caacctcaac 300
186 tcggcgctgg atgcgctgc cgggtgtcctg cccaccttcc cggatgacgc caaacttaca 360
188 aagatcgaga ccctgcgctt cgcccacaac tacatctggg cactgactca gacgtgcgc 420
190 atagcggacc acagcttcta tggcccggag cccctgtgc cctgtggaga gctggggagc 480
192 cccggagggtg gctccaacgg ggactggggc tctatctact cccagtcct ccaagcgggt 540
194 aacctgagcc ccacggcctc attggaggaa ttccctggcc tgcaggtgcc cagctcccca 600
196 tcctatctgc tcccgggagc actggtgttc tcagaactct tgtga 645
199 <210> SEQ ID NO: 5
200 <211> LENGTH: 214
201 <212> TYPE: PRT
202 <213> ORGANISM: MOUSE
204 <400> SEQUENCE: 5
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207 1 5 10 15
209 Thr Gln Gln Pro Phe Pro Gly Ala Ser Asp His Glu Val Leu Ser Ser
210 20 25 30
212 Asn Ser Thr Pro Pro Ser Pro Thr Leu Ile Pro Arg Asp Cys Ser Glu
213 35 40 45
215 Ala Glu Val Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
216 50 55 60
218 Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
219 65 70 75 80
221 Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
222 85 90 95
224 His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
225 100 105 110
227 Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
228 115 120 125
230 His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His

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231      130      135      140
233 Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser
234 145      150      155      160
236 Pro Gly Gly Gly Ser Asn Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
237      165      170      175
239 Ser Gln Ala Gly Asn Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
240      180      185      190
242 Gly Leu Gln Val Pro Ser Ser Pro Ser Tyr Leu Leu Pro Gly Ala Leu
243      195      200      205
245 Val Phe Ser Asp Phe Leu
246      210
248 <210> SEQ ID NO: 6
249 <211> LENGTH: 1412
250 <212> TYPE: DNA
251 <213> ORGANISM: MOUSE
253 <400> SEQUENCE: 6
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256 gcgacacatc tggagccgcg taggatgttc gtcaaattctg agactctgga gttgaaggag      120
258 gaagaggagg tactgatgct gctgggctcg gcttcccccg cctcggcgac cctgaccccg      180
260 atgtcctcca gcgcggacga ggaggaggac gaggagctgc gccggccggg ctccgcgcgt      240
262 gggcagcgtg gagcggaagc cgggcagggg gtgcagggca gtccggcgtc gggtgccggg      300
264 ggttgccggc cagggcggct gctgggcctg atgcacgagt gcaagcgtcg cccgtcgcgc      360
266 tcacgggccc tctcccagg tgccaagacg gcggagacgg tgcagcgcat caagaagacc      420
268 cgcaggctca aggccaacaa ccgcgagcgc aaccgcatgc acaacctaaa cgccgcgctg      480
270 gacgcgctgc gcgaggtgct gcccaccttc cccgaggatg ccaagctcac gaagatcgag      540
272 acgctgcgct tcgcccacaa ttacatctgg gcgctcaccg agactctgcg cctggcggac      600
274 cactgcgcgc gcgcgggttg cctccagggg gcgctcttca cggaggcggg gctcctgagc      660
276 ccgggagctg cgtcgcggcg cagcggggac agcccttctc caccttctct ctggagctgc      720
278 accaacagcc cggcgtcatc ctccaaactc acgtccccat acagctgcac tttatcgccc      780
280 gctagccccc ggtcagacgt ggactactgg cagccccac ctccggagaa gcatcggtat      840
282 gcgcctcacc tgcccctcgc cagggactgt atctagagct gcgggtctcc ctctctcgtc      900
284 ctctaccocg ccctcttccc atccttctcc cgcctctcac cctccacgcc ccggactcca      960
286 cttcacagag cagaggtggc ccttgcaatc ccctcggcg ctggtgcatt cgggggtgga      1020
288 gaccagctct ggtttattga agatgtgagg atttatggtc aaagaggact atggcgtgtg      1080
290 ggagtggggg ctggcggtgg gaacctcgta agactgtaaa agacactgag aaaaagtacc      1140
292 ataactaacg agtgtgcaga gcagactgac gctcctcccc tctctcagag ctgctggagg      1200
294 agaactccgg gcaggcagtt cgtgtgaatc tctcagaggg aatgcaactg gtccctgtga      1260
296 tcttttcacc ttcgtttcta catagagatg ttaatgtcag tcgaaagaaa tgtattttag      1320
298 catctgaatg aatttactgg taataatatt atccacacat ttgcaatggc tggcatctgc      1380
300 tctattccca ttgctgtctg caggctgtgg ga      1412
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304 <211> LENGTH: 263
305 <212> TYPE: PRT
306 <213> ORGANISM: MOUSE
308 <400> SEQUENCE: 7
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311 1      5      10      15
313 Leu Met Leu Leu Gly Ser Ala Ser Pro Ala Ser Ala Thr Leu Thr Pro
314      20      25      30

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316 Met Ser Ser Ser Ala Asp Glu Glu Glu Asp Glu Glu Leu Arg Arg Pro
317 35 40 45
319 Gly Ser Ala Arg Gly Gln Arg Gly Ala Glu Ala Gly Gln Gly Val Gln
320 50 55 60
322 Gly Ser Pro Ala Ser Gly Ala Gly Gly Cys Arg Pro Gly Arg Leu Leu
323 65 70 75 80
325 Gly Leu Met His Glu Cys Lys Arg Arg Pro Ser Arg Ser Arg Ala Val
326 85 90 95
328 Ser Arg Gly Ala Lys Thr Ala Glu Thr Val Gln Arg Ile Lys Lys Thr
329 100 105 110
331 Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu
332 115 120 125
334 Asn Ala Ala Leu Asp Ala Leu Arg Glu Val Leu Pro Thr Phe Pro Glu
335 130 135 140
337 Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr
338 145 150 155 160
340 Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly
341 165 170 175
343 Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser
344 180 185 190
346 Pro Gly Ala Ala Leu Gly Ala Ser Gly Asp Ser Pro Ser Pro Pro Ser
347 195 200 205
349 Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser
350 210 215 220
352 Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp
353 225 230 235 240
355 Tyr Trp Gln Pro Pro Pro Glu Lys His Arg Tyr Ala Pro His Leu
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358 Pro Leu Ala Arg Asp Cys Ile
359 260
361 <210> SEQ ID NO: 8
362 <211> LENGTH: 1957
363 <212> TYPE: DNA
364 <213> ORGANISM: MOUSE
366 <400> SEQUENCE: 8
367 gatacacaca gatctagagg ctccaggaga cgatgcgaca ctcagcctga aaagatttgg 60
369 aagatccaaa atgaaaactg attattgaat gaaattaaaa cctaaggtaa attaagggtta 120
371 aagaaccatg ttaacactac cgtttgacga gtctgtcgta atgcccgaat cccagatgtg 180
373 cagaaagttt gctagacaat gtgaggacca gaaacaaatt aagaaaccag agagctttcc 240
375 aaaacaagtt gtccttcgag gaaagagcat taaaagggcc cctggagaag aaaccgagaa 300
377 agaagaggag gaagaagaca gagaggaaga agatgagaat ggcttggtcca gaaggagggg 360
379 gctcaggaaa aaaaagacca ccaaactacg actggaaagg gtcaagttca ggagacagga 420
381 agctaattgc gcgagagga accggatgca cggcctcaat gatgctctgg acaatttgcg 480
383 aaaagtggtc ccctgttact ctaaaacca aaaactgtcc aaaatagaaa ctttacgact 540
385 ggccaaaaat tacatctggg cactttctga aattctgagg attggcaaga gaccggatct 600
387 gctcacgttc gtccaaaact tatgcaaagg tctttcccag ccaactacaa acttggtggc 660
389 aggtctgtta cagctcaacg ccagaagttt cctgatgggt caggggtggg aggtgcccac 720
391 ccacacaagg tcaccctact ccacattcta cccaccctac cacagccctg agctggccac 780
393 tccccaggg catgggactc ttgataattc caagtccatg aaaccctaca attactgcag 840

→ Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

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